Supplementary Information for:

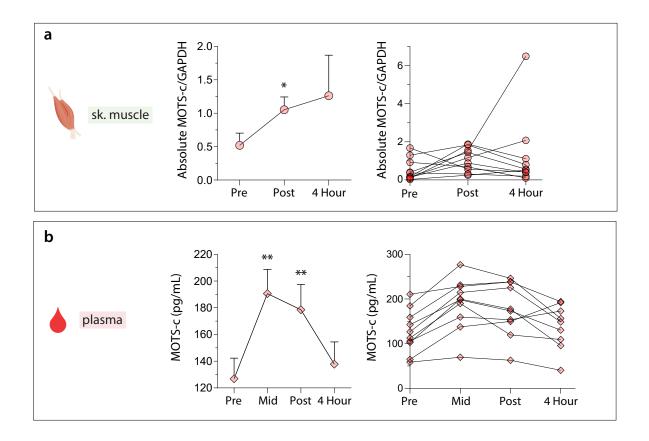
MOTS-c is an Exercise-Induced Mitochondrial-Encoded Regulator of Age-Dependent Physical Decline and Muscle Homeostasis

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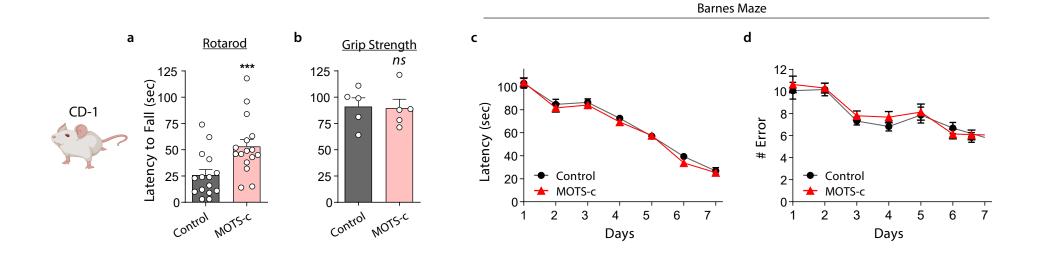
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This file includes Supplementary Figures 1-18.

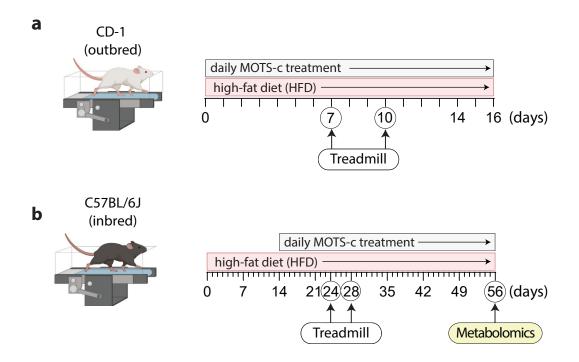


Supplementary Figure 1. Absolute MOTS-c levels in human muscle and plasma.

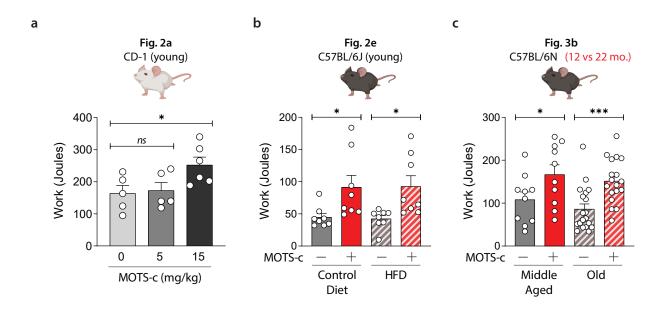
Relative MOTS-c levels are shown in Fig. 1c-d. Here, the absolute quantification of MOTS-c levels measured by **a** Western blotting on human skeletal muscle collected pre-, post-exercise and 4-hours of resting, normalized to corresponding GAPDH levels (MOTS-c/GAPDH) (P=0.0098) and **b** ELISA on plasma from the same individuals collected pre-, mid-, post-exercise and 4-hours of resting (n=10) (P=0.0011 Mid-; P=0.0020 Post-exercise). Data are presented as both average values and individual datapoints. Statistics by Wilcoxon matched-pair signed rank test. *P<0.005 **P<0.01.



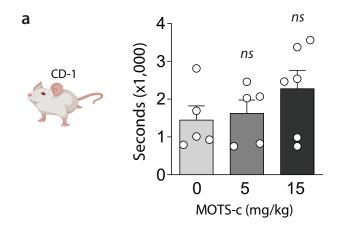
Supplementary Figure 2. Rotarod, grip strength, and Barnes Maze tests in MOTS-c treated old mice. a Summary of latancy time to fall on the Rotarod test (n=13 Control, n=16 MOTS-c) (P=0.0042). The speed of the rotations increased from a starting speed of 24 rpm by 1 rpm every 10 seconds. **b** Grip strength test (n=5) (P=0.7012). **c**, **d** Barnes Maze performance in control and MOTS-c treated 12-week old mice (n=15). **c** There was no change in the average time to find the escape box (latency) between control and MOTS-c treated mice. **d** There was no change in the number of errors made prior to discovering the escape box between groups. Errors were defined as nose-pokes or head deflections over false holes. Data expressed as mean +/- SEM of three 24-hour acquisition cycles. Two-sided Student's t-test. *P<0.05. **P<0.001, ***P<0.0001.

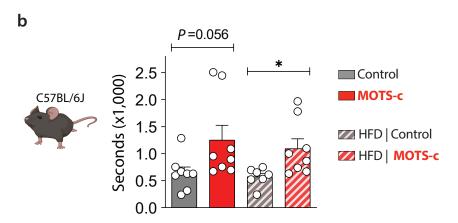


Supplementary Figure 3. Outline of HFD mouse experiments. Timeline of experiment for 12-week old male CD-1 (outbred) and C57BL/6J (inbred) mice fed a HFD or defined control diet. **a** CD-1 mice were fed a HFD and given daily intraperitoneal injections (IP) of MOTS-c (0, 5, or 15 mg/kg/day) from Day 0. Treadmill running tests were performed on Day 7 (Supplementary Fig. 5a) and Day 10 (Fig. 2a-d). Daily MOTS-c injections ceased at Day 16. **b** C57BL/6J mice were started on either a HFD or a defined control diet on Day 0 and continued uninterruptedly throughout the experiment. Daily MOTS-c treatment (15 mg/kg; IP) started on Day 14. Treadmill running tests were performed on Day 24 and Day 28 (10 days and 14 days after the start of MOTS-c treatment) (Fig. 2e-h; Supplementary Fig. 5b). Mice were treated daily until Day 56, at which time metabolomics was performed (Fig. 2i).

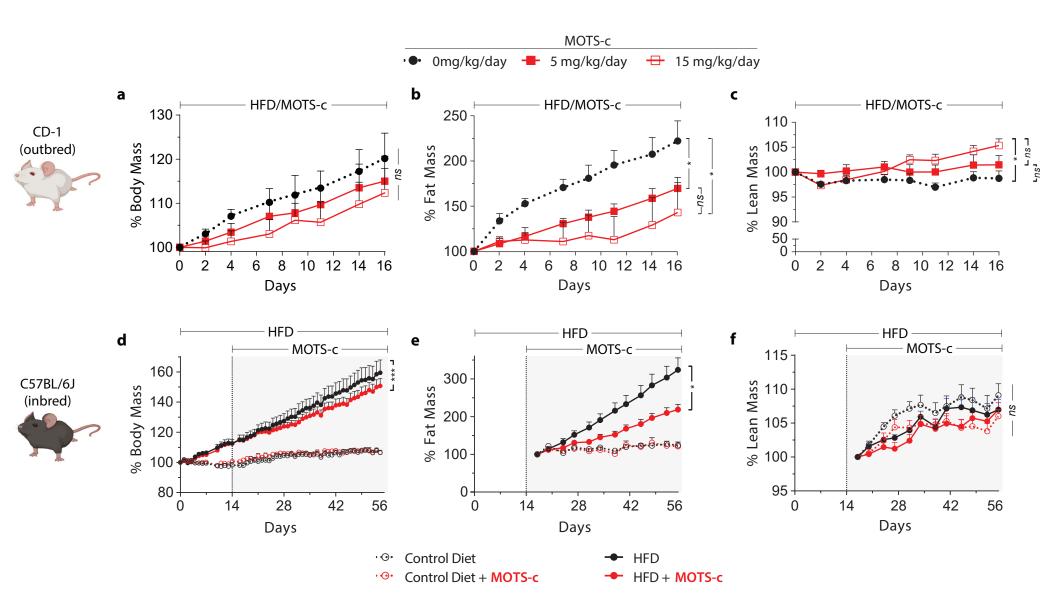


Supplementary Figure 4. The effect of MOTS-c on exercise work output. Based on the treadmill running studies in **a** young CD-1 (Fig. 2a) (n=5 0,5 mg/kg MOTS-c, n=6 15mg/kg MOTS-c) (P=0.0346), **b** C57BL/6J (Fig. 2e) (n=8) (P=0.0286 control diet; P=0.0122 HFD), and **c** middle-aged and old C57BL/6N mice (Fig. 3b) (n=10 Middle-Aged mice, n=18 Old MOTS-c and n=19 Old Control) (P=0.0479 Middle-Aged and P=0.0005 Old), total exercise work output was calculated taking into account body weight, acceleration due to gravity, and distance. Data expressed as mean +/- SEM. Two-sided Student'ds t-test *P<0.05, ****P<0.0001.

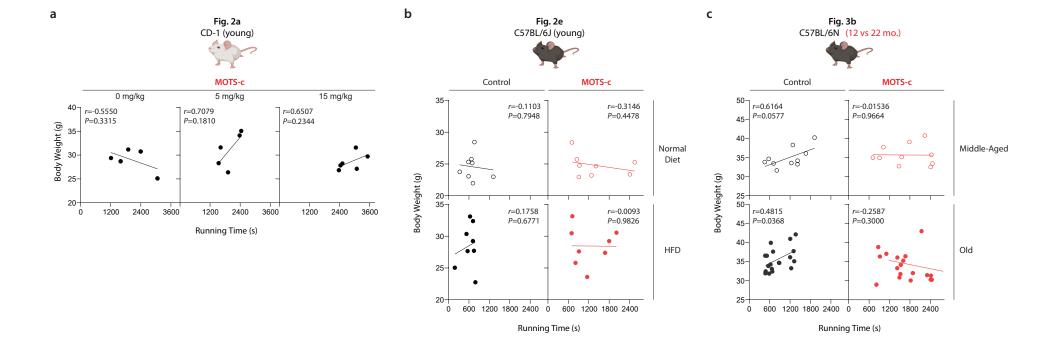




Supplementary Figure 5. Initial running time of MOTS-c treated young mice. a Running time of CD-1 mice following seven days of MOTS-c treatment (n=5 for Control and 5 mg/kg MOTS-c, n=6 for 15 mg/kg MOTS-c). MOTS-c (15mg/kg/day) treatment showed a trend towards enhanced running performance. **b** Running time of HFD-fed C57BL/6J mice following 10 days of MOTS-c treatment (n=8) (*P*=0.0229). Data expressed as mean +/- SEM. Two-sided Student's t-test. **P*<0.05

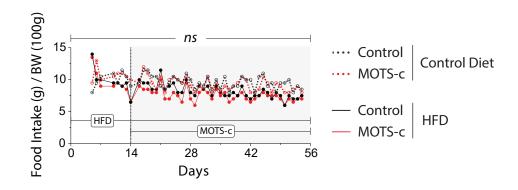


Supplementary Figure 6. Body composition analysis on MOTS-c treated young mice. Body composition was measured non-invasively using a time-domain NMR analyzer. **a-c** Young CD-1 mice were treated daily with MOTS-c (0, 5, or 15 mg/kg/day;IP) for 16 days (n=5 control and 5 mg/kg/day MOTS-c, n=6 for 15 mg/kg/day MOTS-c and percent **a** body weight, **b** fat mass (*P*=0.0320, 5 vs. 15; *P*=0.0251, 0 v 15), and **c** lean muscle mass (*P*=0.0105) were measured. **d-f** C57BL/6J mice either on a HFD or a defined Control Diet and treated daily with MOTS-c (15 mg/kg/day;IP) or saline control (n=8) and percent **d** body weight (*P*<1E-15), **e** fat mass (*P*=0.0119), and **f** lean muscle mass were measured. The dotted line at Day 14 represents the start of MOTS-c treatment. Data expressed at mean +/- SEM. Significance determined using two-wat ANOVA (repeated measures). **P*<0.05, ***P*<0.001, ****P*<0.0001.



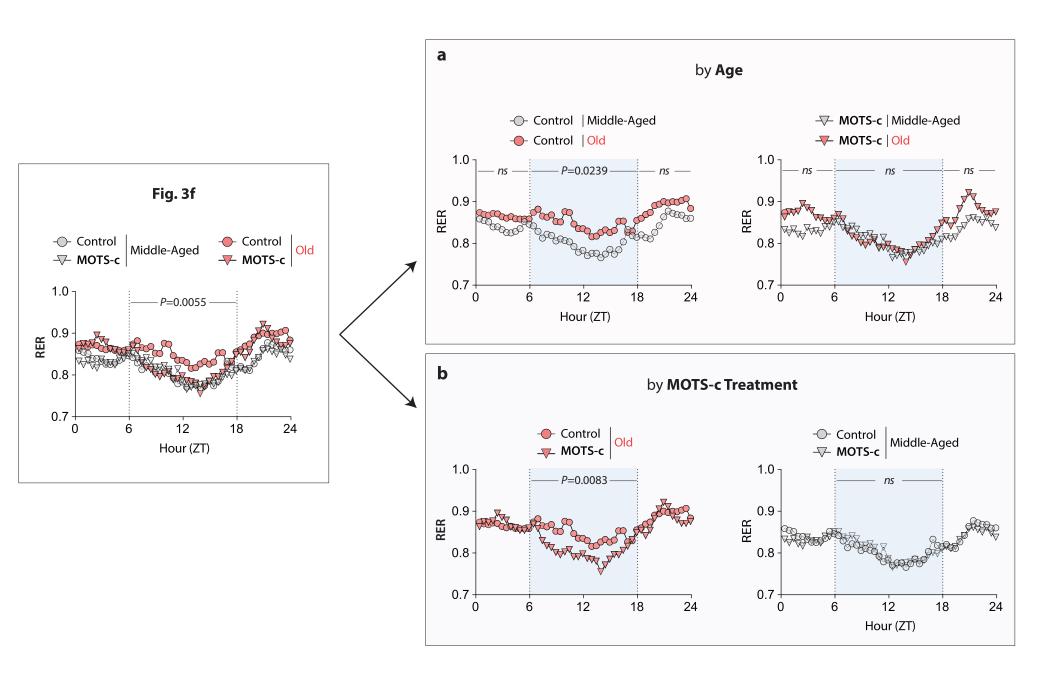
Supplementary Figure 7. Correlation between body weight and running capacity.

Correlation between body weight (g) and running time (s) was calculated based on Pearson correlation coefficient for **a** young CD-1 (see Fig. 2a), **b** young C57BL/6J (see Fig. 2e), and **c** older C57BL/6N (see Fig. 3b) mice.

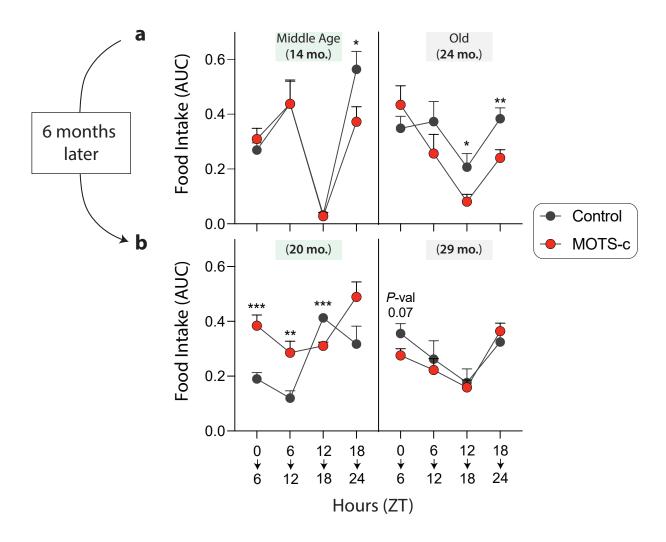


Supplementary Figure 8. The effect of MOTS-c on food intake in young C57BL/6J mice fed a normal or high-fat diet. Young C57BL/6J mice either on a HFD or a defined control diet were treated daily with MOTS-c (15 mg/kg/day; IP) or saline control (n=8) and food intake was measured. Mice were housed 4 animals/cage and food weight was measured per cage. Food intake is presented per mouse. Two-way ANOVA on 2 cages/group. The dotted line at Day 14 represents the start of MOTS-c treatment. Related to Fig. 2e-i.

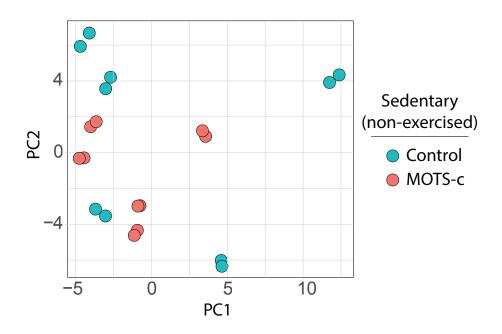
Supplementary Figure 9. Principal component loadings. PC loading **a** relevant to Fig. 2i, PC1 PC3 scatter plot with Glycolysis/ Pentose Phosphate Pathway labels and **b** relevant to Fig. 3g, PC1 PC2 scatter plot with Glycolysis and Hydrophobic Amino Acid labels.



Supplementary Figure 10. Alternate presentation of Fig. 3f divided by age and MOTS-c treatment. P-values derived using two-way ANOVA. **a** P=0.0239. **b** P=0.0083.



Supplementary Figure 11. Circadian pattern of food intake in MOTS-c treated old mice. a The sum of coninuous food intake measurements using metabolic cages divided into daily quartiles in MOTS-c treated middle-age (14 months) (P=0.0359) and old (24 months) (P=0.0370 and P=0.0089, respectively) mice (n=4). **b** Measurements were taken six months later in the same mice (P=0.0004, 0-6. P=0.0031, 6-12. P=0.000025, 12-18 and P=0.057 18-24). Data expressed as mean +/- SEM. Two-sided Student's t-test. *P<0.05, **P<0.01, ***P<0.001.



Supplementary Figure 12. Metabolomic analysis on sedentary MOTS-c-treated old mice. Skeletal muscle from sedentary (not treadmill-exercised) old mice (22.5 months) treated daily with MOTS-c (15 mg/kg/day) for 2 weeks (n=10) were subject to metabolomics and analyzed using PCA.

Pathways (GSEA/GO_Biological Process)

signed

enrichment

20

1.8

1.6

1.4

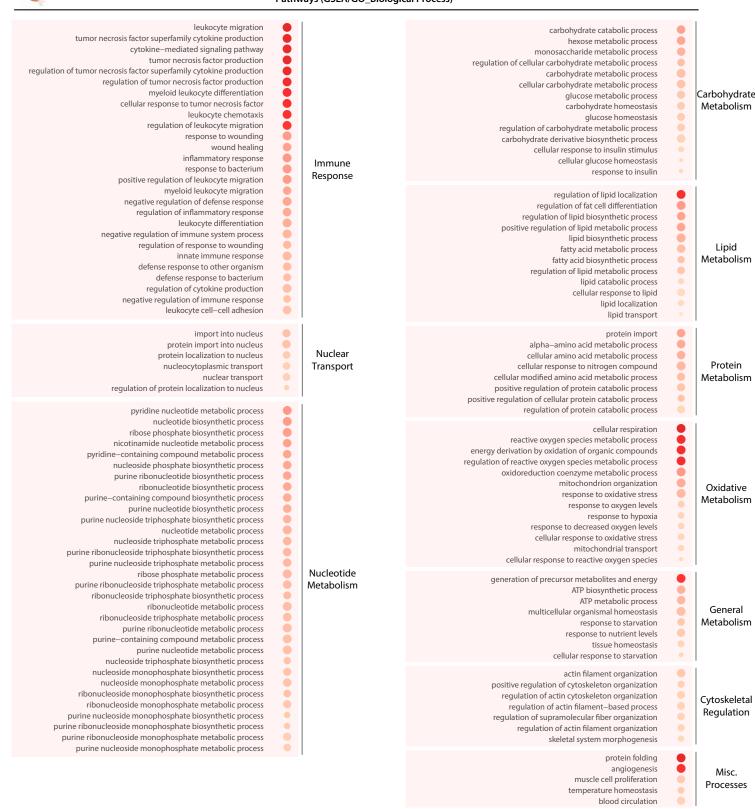
Pval

(-Log10)

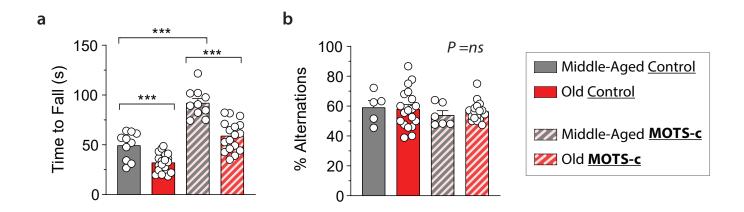
1.0

1.2

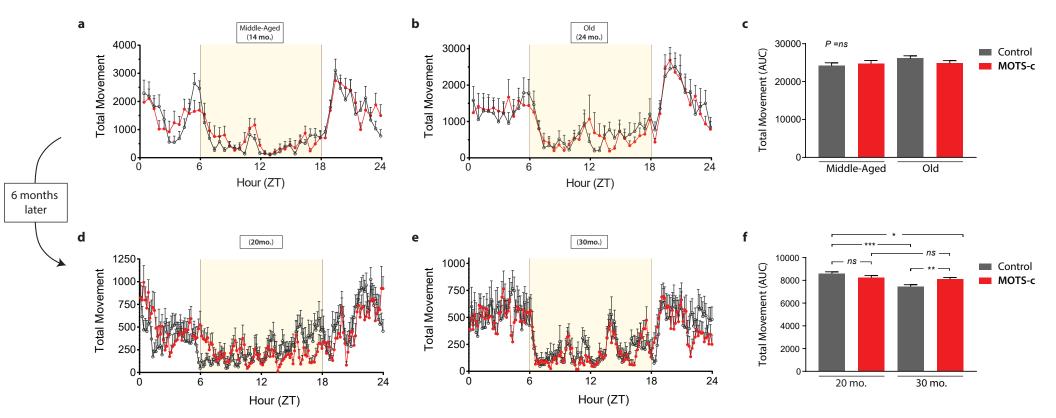
1.4



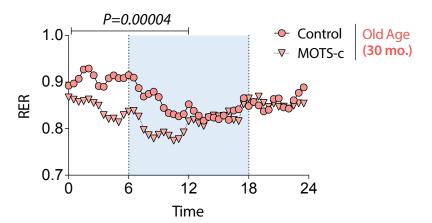
Supplementary Figure 13. Gene expression analysis on skeletal muscle from exercised MOTS-c-treated old mice. RNA-seq was performed on skeletal muscles from MOTS-c-treated old mice. Balloon plots of biological processes derived from Gene Set Enrichment Analysis (GSEA) using the Gene Ontology (Biological Process) database at a false discovery rate (FDR) < 15% (n=6).



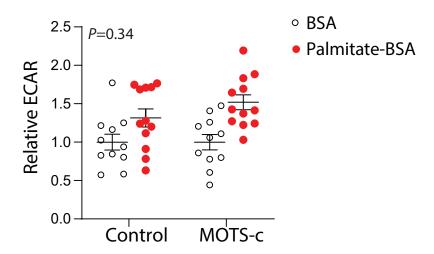
Supplementary Figure 14. Rotarod and Y-Maze tests in MOTS-c treated old mice. Middle-aged (14 mo.) and old (24 mo.) mice (n=10 middle-aged mice; n=17 old MOTS-c and n=19 old Control) were treated daily with MOTS-c (15 mg/kg/day;IP) and subject to **a** a rotarod test (*P*=0.000442, MA Control vs. Old Control, *P*=0.000008, MA MOTS-c vs. Old MOTS-c, *P*=0.000003, MA Control vs. MA MOTS-c, and *P*=0.0000002, Old Control vs. Old MOTS-c) and **b** y-maze test. Data expressed as mean +/- SEM. Two-sided Student's t-test. ***P<0.0001.



Supplementary Figure 15. Total Physical Activity in MOTS-c treated old mice. Total movement [horizontal and vertical movement (XYZ-axis)] of MOTS-c treated a middle-aged (14 mo.) and b old (24 mo.) mice were continuously measured using metabolic cages throughout the day for three days (n=4). c The sum of all measured movements is shown. d-f The procedure was repeated on the same mice after 6 months of LLII MOTS-c treatment (*P*=0.0029, Old Control vs. Old MOTS-c, *P*=0.026, Middle-Aged Control vs. Old MOTS-c, *P*=0.000013, Middle-Aged Control vs. Old Control. Data expressed as mean +/- SEM of three 24-hour acquisition cycles. Two-sided Student's t-test. **P*<0.05, ****P*<0.001, *****P*<0.0001.



Supplementary Figure 16. MOTS-c-dependent circadian fuel selection old mice. Respiratory Exchange Ratio (RER) measurements in LLII MOTS-c-treated, or control, old mice (30 mo.; n=4). Shaded region represents daytime (light cycle) (*P*=0.00004). Data expressed as mean +/- SEM of three 24-hour acquisition cycles. Two-way ANOVA (repeated measures).



Supplementary Figure 17. MOTS-cdependent glycolytic rate in lipid-stimulated mouse myoblasts. C2C12 mouse myoblasts were treated with MOTS-c (10uM) or saline control in nutruent-limited media (n=11 BSA baseline, n=12 palmitate addition). Real-time glycolytic flux determined by the extracellular acidification rate was measured using the XF96 Seahorse bioanalyzer. Prior to the start of the assay, nutrient-deprived cells were given either BSA alone or palmitate bound to BSA (palmitate-BSA) to determine the capacity to metabolize fatty acids. Data expressed as mean +/- SEM. Two-Way ANOVA. *P<0.05, **P<0.01,***P<0.001.

Pathways (GO_BP) protein folding ribosome biogenesis response to topologically incorrect protein regulation of ubiquitin-dependent protein catabolic process rRNA processing ribonucleoprotein complex biogenesis mRNA processing regulation of proteolysis involved in cellular protein catabolic process regulation of proteasomal protein catabolic process regulation of mRNA processing negative regulation of proteolysis proteasome-mediated ubiquitin-dependent protein catabolic process regulation of cellular protein catabolic process mRNA metabolic process protein stabilization RNA splicing RNA splicing, via transesterification reactions \bigcirc RNA splicing, via transesterification reactions with bulged adenosine as nucleophile Protein mRNA splicing, via spliceosome Translation regulation of mRNA metabolic process proteasomal protein catabolic process 0 Regulation regulation of protein catabolic process rRNA metabolic process RNA localization modification-dependent protein catabolic process ubiquitin-dependent protein catabolic process regulation of protein modification by small protein conjugation or removal regulation of protein ubiquitination 0 regulation of proteolysis positive regulation of protein catabolic process negative regulation of protein modification process negative regulation of phosphorylation negative regulation of protein phosphorylation positive regulation of establishment of protein localization regulation of establishment of protein localization proteolysis involved in cellular protein catabolic process extrinsic apoptotic signaling pathway intrinsic apoptotic signaling pathway regulation of intrinsic apoptotic signaling pathway apoptotic signaling pathway negative regulation of apoptotic signaling pathway \bigcirc Cell Death regulation of neuron death regulation of neuron apoptotic process neuron death regulation of apoptotic signaling pathway 0 positive regulation of programmed cell death 0 positive regulation of apoptotic process 0 response to oxidative stress 0 **Oxidative Stress** response to reactive oxygen species cellular response to oxidative stress 0 0 nucleocytoplasmic transport **Nuclear Transport** nuclear transport cellular response to hormone stimulus response to hormone Response to Hormones cellular response to steroid hormone stimulus 0 regulation of cellular catabolic process modification-dependent macromolecule catabolic process positive regulation of cellular catabolic process 0 positive regulation of catabolic process Misc. Catabolic Processes cellular nitrogen compound catabolic process 0 organic cyclic compound catabolic process heterocycle catabolic process response to lipid negative regulation of phosphorus metabolic process 0 Misc. Metabolic Processes

signed

enrichment

2.2

20

1.8

16

Pval

(-Log10)

• 1.35

1.40

1.45

negative regulation of phosphate metabolic process